REMARKS

The present Amendment is in further response to the Examiner's Office Action mailed November 26, 2003 and Applicants' telephone interviews with Examiner Teresa D. Wessendorf on April 7, 2004, with Examiners Wessendorf and Andrew Wang on May 24, 2004, and with Examiner Teresa D. Wessendorf on July 2, 2004. Claims 5-7 and 18 are canceled. Claim 1 is amended. Claims 1-4, 8-17, and 19 are now pending.

Applicants express their appreciation to the Examiners Wessendorf and Wang for conducting telephone interviews with Applicants. During the interview, Applicants distinguished the claimed invention from the disclosure of Weissman et al. (U.S. Patent No. 6,066,452) cited by the Examiner in the rejection under 35 U.S.C §103(a).

As discussed during the interviews, the present invention is a method of identifying a transcription factor modulator by using a library of nucleic acid probes each of which comprises a recognition sequence **that is known to bind to an activated known transcription factor (TF) and varies within the library for binding to different activated known transcription factors.** By using such a library of TF probes multiple, different activated TFs in a sample can be identified efficiently, and preferably simultaneously. By comparing the profile of activated TFs of a test sample treated with an agent with that of an untreated control sample, the agent that causes a difference in the profile of the test sample is identified as a transcription modulator.

In contrast, Weissman et al. discloses a method for identifying **new pairs of transcription factor-DNA binding sites** by using a library of nucleic acid probes with randomized sequences. Column 2, lines 4-15. Weissman et al. neither teaches nor suggests using a library of nucleic acid probes, each of which is already known to bind to a known transcription factor, to identify activated transcription factor, let alone teach or suggest using such a library of probes to identify transcription modulators. Further, if Weissman et al. used the library of nucleic acid probes as claimed by Applicants, their purpose of finding new transcription factors would be defeated because the probes are already known to bind to known transcription factors. Based on these reasons, Applicants respectfully traverse the Examiner's grounds for rejecting the claims.

However, in an effort to advance prosecution of this application and without acquiescing to the propriety of this rejection Applicants amend independent Claim 1 to specify that the nucleic acid probes in the library are capable of binding to at least two activated transcription

factors selected from the group consisting of AP1, AP-2, ARE, Brn-3, C/EBP, CBF, CDP, c-Myb, CREB, E2F-1, EFR, ERE, Ets, Ets-1/PEA3, FAST-1, GAS/ISRE, GATA, GRE, HNF-4, IRF-1, MEF-1, MEF-2, Myc-Max, NF-1, NFATc, NF-E1, NF-E2, NF.kappa.B, Oct-1, p53, Pax-5, Pbx1, Pit 1, PPAR, PRE, RAR, RAR (DR-5), SIE, Smad SBE, Smad3/4, SP1, SRE, Stat1, Stat3, Stat4, Stat4, Stat5, Stat6, TFIID, TR, TR(DR-4), USF-1, VDR (DR-3), HSE, and MRE.

In view of the distinct differences between claimed method and that disclosed in Weissman et al., the claimed invention is non-obvious under 35 U.S.C. §103(a). Withdrawal of the rejection is therefore respectfully requested.

CONCLUSION

In light of the remarks and arguments set forth above, Applicants earnestly believe that they are entitled to a letters patent, and respectfully solicit the Examiner to expedite prosecution of this patent application to issuance. Should the Examiner have any questions, the Examiner is encouraged to telephone the undersigned.

Respectfully submitted,

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Shirley Chen, Ph.D.
Registration No. 44,608

WILSON SONSINI GOODRICH & ROSATI
650 Page Mill Road
Palo Alto, CA 94304-1505
Direct line: (650) 565-3856
Client No. 021971